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============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2010; month=7; day=27; hr=11; min=15; sec=3; ms=141; ]
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Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15                  20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                 35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
             50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
         65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
     80                  85                  90

Please remove the blank line between the above row of codons and their
respective amino acids; the amino acids should appear directly below
their their codons.
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<210> 15
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

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Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

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                35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
            50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
    80                  85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct   339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95                  100                 105                 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc   387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115                 120                 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act   435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
            130                 135                 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac   483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
        145                 150                 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa   531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
    160                 165                 170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt   579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                 180                 185                 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att   627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
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                195                 200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt   675
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gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct   723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
        225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat   771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
    240                 245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat   819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
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Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
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gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc   915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta   963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
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aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
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                355                 360                 365
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ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
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415                 420                 425                 430

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ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
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agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
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atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                     1576
Asn Asp Gly Ser Val Ile
                515
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1) Please remove the blank line between the above row of codons and their amino acids; 2) the above <220>-<223> section describing "k" at

location 1578 is incorrect; the sequence only has 1576 nucleotides. Same errors in Sequences 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39 and 41.

<210> 33
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 33
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1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

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 15                  20                  25                  30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35                  40                  45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
            50                  55                  60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65                  70                  75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
    80                  85                  90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct   339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95                 100                 105                 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc   387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                115                 120                 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act   435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
            130                 135                 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac   483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
        145                 150                 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa   531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
    160                 165                 170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt   579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175                 180                 185                 190
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```
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att   627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195                 200                 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt   675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
            210                 215                 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct   723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
        225                 230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat   771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
    240                 245                 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat   819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260                 265                 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat   867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                 280                 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc   915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
            290                 295                 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta   963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
        305                 310                 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat atg agt   1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser
    320                 325                 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc   1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
```

```
                355                 360                 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc   1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
            370                 375                 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
        385                 390                 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
    400                 405                 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                 420                 425                 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                 440                 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
            450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
        465                 470                 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                      1576
Asn Asp Gly Ser Val Ile
                515
```

Two errors above: 1) the <220>-<223> section describing the "y" at location 1008 is errored: "g" is at locadtion 1008; 2) the <220>-<223> section describing the "k" at location 1578 is errored: there are only 1576 nucleotides above.

****

Validated By CRFValidator v 1.0.3

Application No: 10569000 Version No: 2.0

Input Set:

Output Set:

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Finished: 2010-07-22 16:44:19.919
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 897 ms
Total Warnings: 0
Total Errors: 112
No. of SeqIDs Defined: 42
Actual SeqID Count: 42

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E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
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E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
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E	336	Empty lines found between the proteins and the dna

Input Set:

Output Set:

Started: 2010-07-22 16:44:17.022
Finished: 2010-07-22 16:44:19.919
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 897 ms
Total Warnings: 0
Total Errors: 112
No. of SeqIDs Defined: 42
Actual SeqID Count: 42

Error code	Error Description
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SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.
Hannah, L. Curtis
Lyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase

<130> UF-371XC1 PCT

<140> 10569000
<141> 2010-07-22

<150> US 60/496,188
<151> 2003-08-18

<160> 42

<170> PatentIn version 3.2

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        35                  40                  45

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Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
                85                  90                  95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
            100                 105                 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
        115                 120                 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
    130                 135                 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
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Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
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Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
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Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
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Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
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Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
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Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
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            340                 345                 350

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    370                 375                 380

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Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
                405                 410                 415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
            420                 425                 430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
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Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile
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Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
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<212> DNA
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attcctgtca gcaattgtct caacagcaac atatccaaga tctatgtgct aacgcaattt 300

aactctgctt ccctcaaccg tcacctctca agagcctacg ggagcaacat tggagggtac 360

aagaatgaag ggtttgttga agtcttagct gcacagcaga gcccagataa tccaaactgg 420

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atggaatttc taattcttgc tggcgatcac ctgtaccgga tggactatga aaagttcatt 540

caggcacaca gagaaacaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa 600

cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgct 660

gagaaaccga aaggagagca gttgaaagca atgatggttg acaccaccat acttggcctt 720

gatgacgtga gggcaaagga aatgccttat attgctagca tgggtatcta tgttttcagc 780

aaagatgtaa tgcttcagct cctccgtgaa caatttcctg aagccaatga ctttggaagt 840

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tactgggaag atatcggtac cattgcggca ttttataatg caaacttggg aataaccaag 960

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<210> 4
<211> 475

<212> PRT
<213> zea mays

<400> 4

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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
            20                  25                  30

Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
        35                  40                  45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
    50                  55                  60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65                  70                  75                  80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
                85                  90                  95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
            100                 105                 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
        115                 120                 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
    130                 135                 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145                 150                 155                 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
                165                 170                 175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
            180                 185                 190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
        195                 200                 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
    210                 215                 220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
225                 230                 235                 240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
                245                 250                 255
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Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
            260                 265                 270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
        275                 280                 285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
    290                 295                 300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
305                 310                 315                 320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
                325                 330                 335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
            340                 345                 350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
        355                 360                 365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
    370                 375                 380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385                 390                 395                 400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
                405                 410                 415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
            420                 425                 430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
        435                 440                 445

Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile
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Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465                 470                 475
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<210> 5
<211> 1428
<212> DNA
<213> zea mays

<400> 5

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caagctcatg atagtgttct tggaatcatt ctgggaggtg gtgctgggac tagattgtac    180

cccttgacaa agaagcgtgc caagcctgca gtgccattgg gtgccaacta tagactgatt    240
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tacaagaatg aagggtttgt tgaagtctta gctgcacagc agagcccaga taatccaaac    420

tggtttcagg gtactgcaga tgctgtaagg cagtacttgt ggttgtttga ggagcataat    480

gtgatggaat ttctaattct tgctggcgat cacctgtacc ggatggacta tgaaaagttc    540

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cttgatgacg tgagggcaaa ggaaatgcct tatattgcta gcatgggtat ctatgttttc    780

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aagaagccaa taccagattt cagcttctat gaccgttttg ctccaattta tacacaacct   1020

cgacacctgc caccttcaaa ggttcttgat gctgatgtga cagacagtgt tattggtgaa   1080

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aatgctgaca atgttcaaga agctgcaatg gagacagacg ggtacttcat caaaggtgga   1380

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<210> 6
<211> 476
<212> PRT
<213> zea mays

<400> 6

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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
            20                  25                  30

Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
```

```
        35                  40                  45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
    50                  55                  60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65                  70                  75                  80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
                85                  90                  95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
            100                 105                 110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
        115                 120                 125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
    130                 135                 140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
145                 150                 155                 160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
                165                 170                 175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
            180                 185                 190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
        195                 200                 205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
    210                 215                 220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
225                 230                 235                 240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
                245                 250                 255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln
            260                 265                 270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
        275                 280                 285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
    290                 295                 300

Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
305                 310                 315                 320

Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
                325                 330                 335

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
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```
            340                 345                 350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
        355                 360                 365

Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
    370                 375                 380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
385                 390                 395                 400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
                405                 410                 415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
            420
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